

## SUBSTITUTE SHEET (RULE 26)



2/30

Earl  
SapI

Earl

600

EEEDTPSVMEEELDKWNNSMNSTNNADFECLPTLKEEKESNHNPSSDSSES

AlwNI BbvCI  
Bsu36I Bpu10I

BamHI

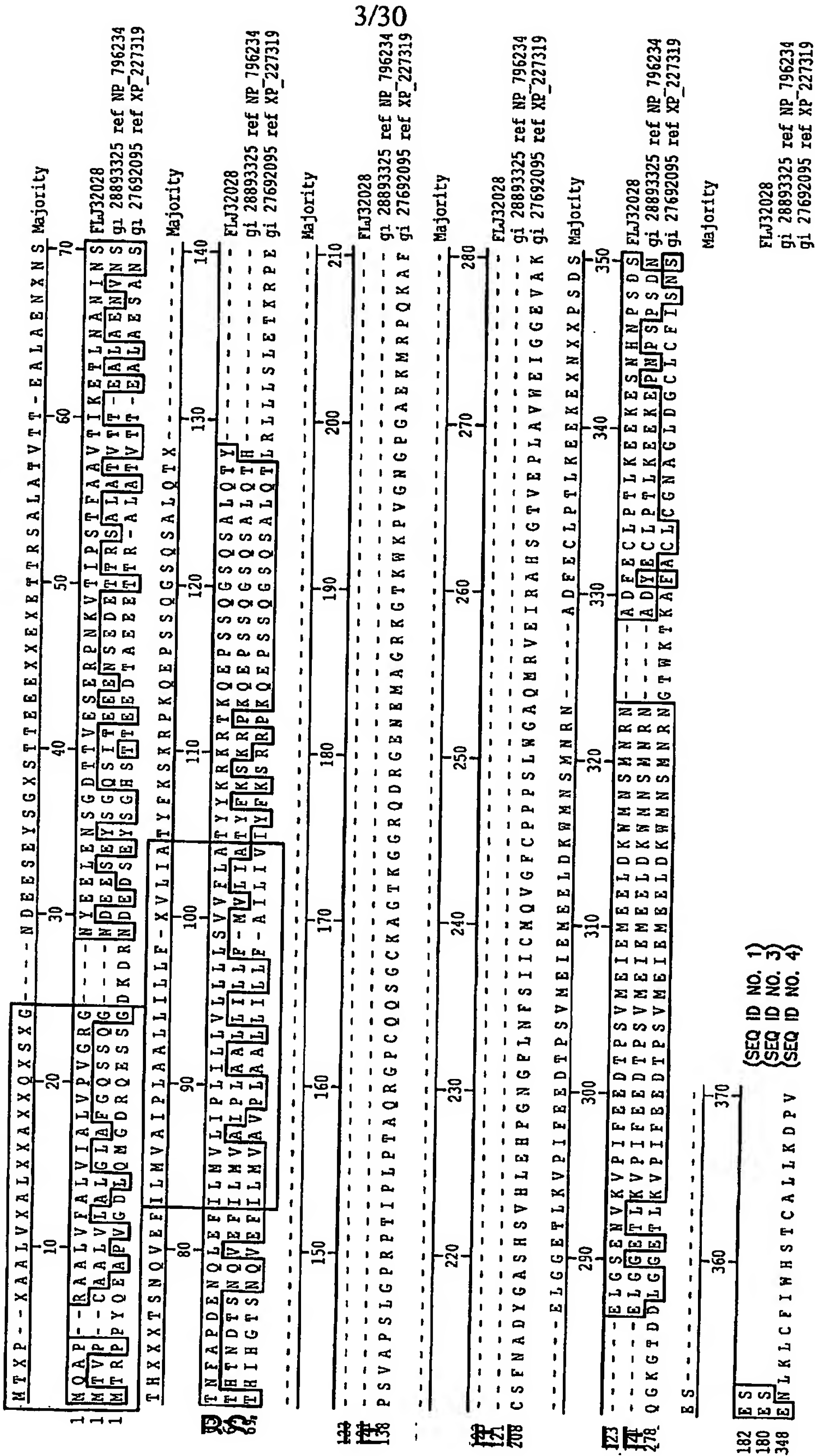
(SEQ ID NO. 2)

676

R1 Primer

**FIG. 1** *con't*

Alignment of Human FLJ32028 Protein with Similar Proteins from Rodents



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FIG. 2

FLJ32028 protein with N-terminal HA Tag

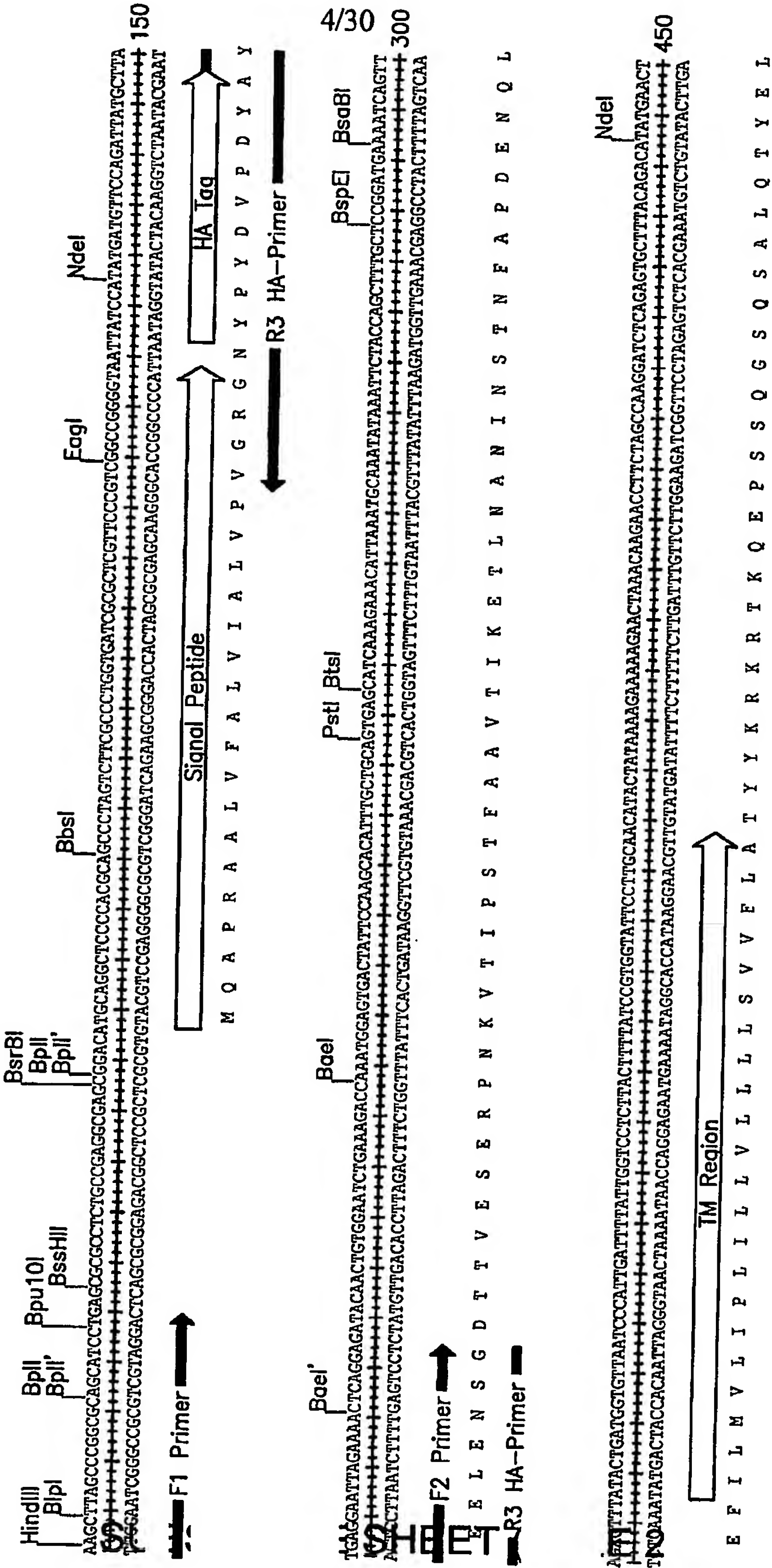


FIG. 3

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Earl  
SapI  
Earl

Bmrl

600

SENVKVP I F E E D T P S V M E I E M E E L D K W M N S M N R N A D F E C L P T L K E E K E S

AlwNI  
Bsu36I  
BbvCI  
Bpu10I  
BamHI

703

(SEQ ID NO. 5)

R1 Primer

CHNPSSSS (SEQ ID NO. 6)

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**FIG. 3 con't**

FLJ32028 Protein with C-terminal HA Tag

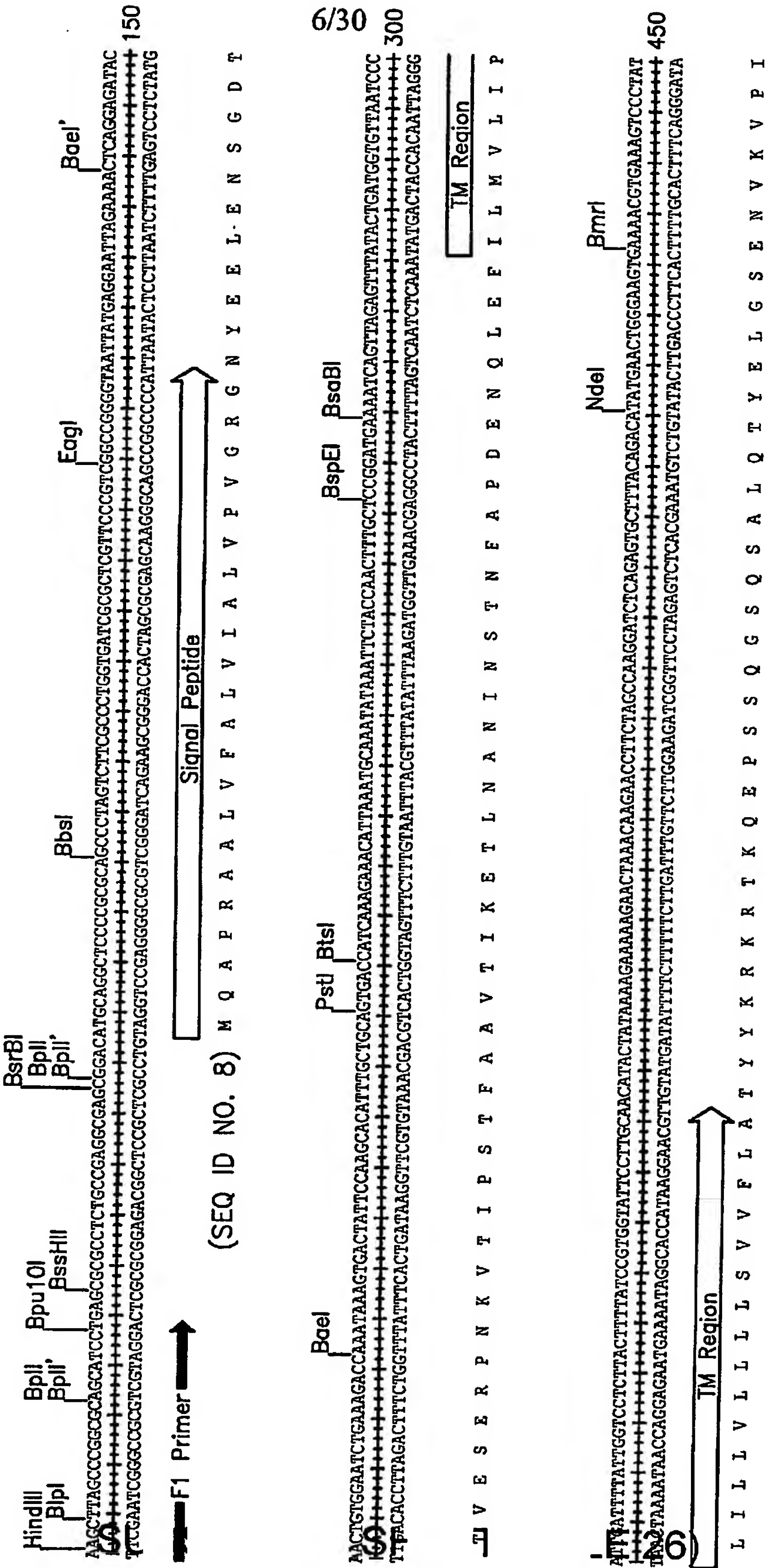


FIG. 4



EarI  
 SspI  
 EarI  
 600  
 7/30  
 R2-HA Primer  
 HA-Tag  
 637 (SEQ ID NO. 7)

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## FACs Analysis of Transfected 293-EBNA Cells

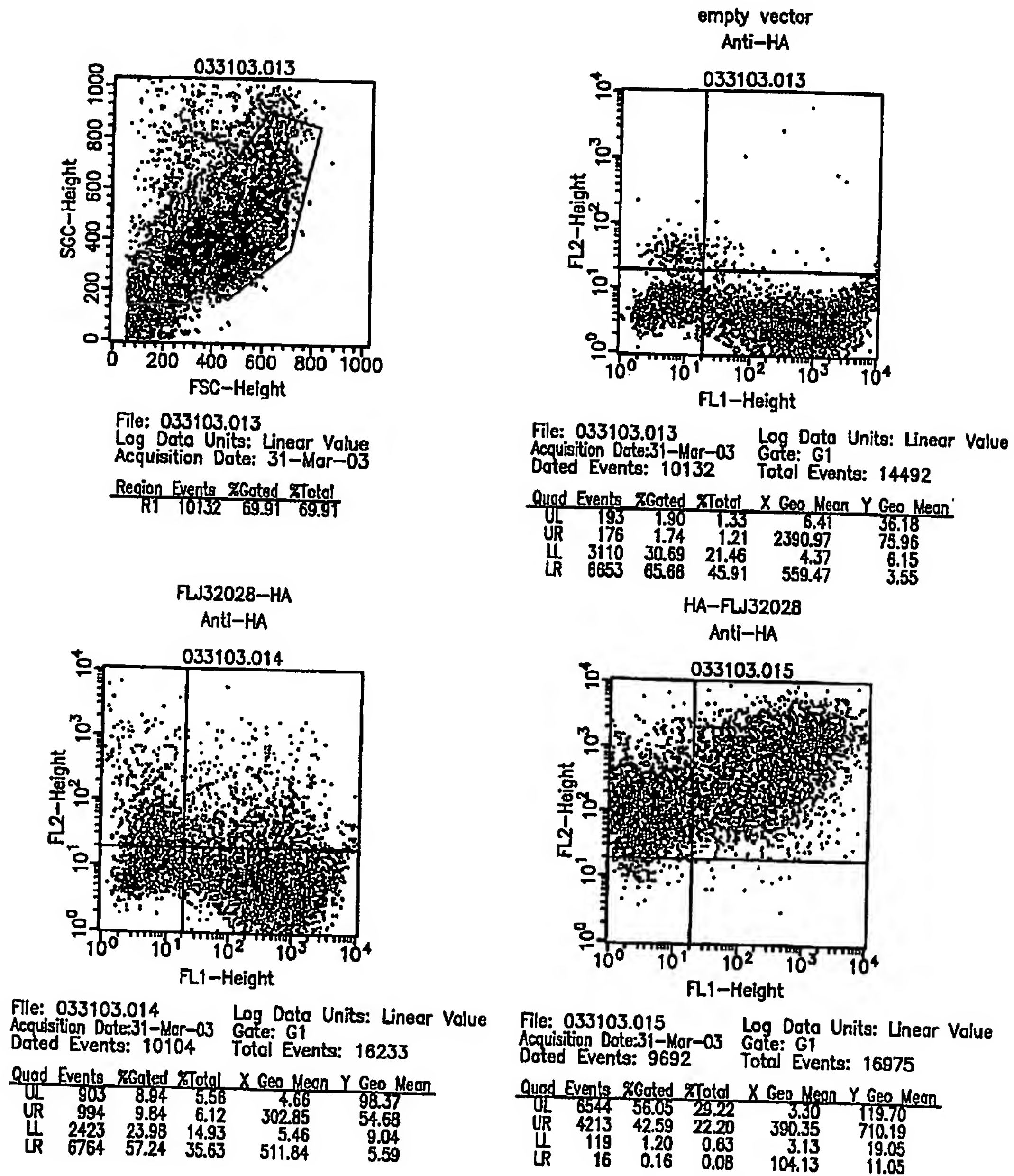


FIG. 5



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# Anti-HA Western Blot of Transfected 293-EBNA Cells

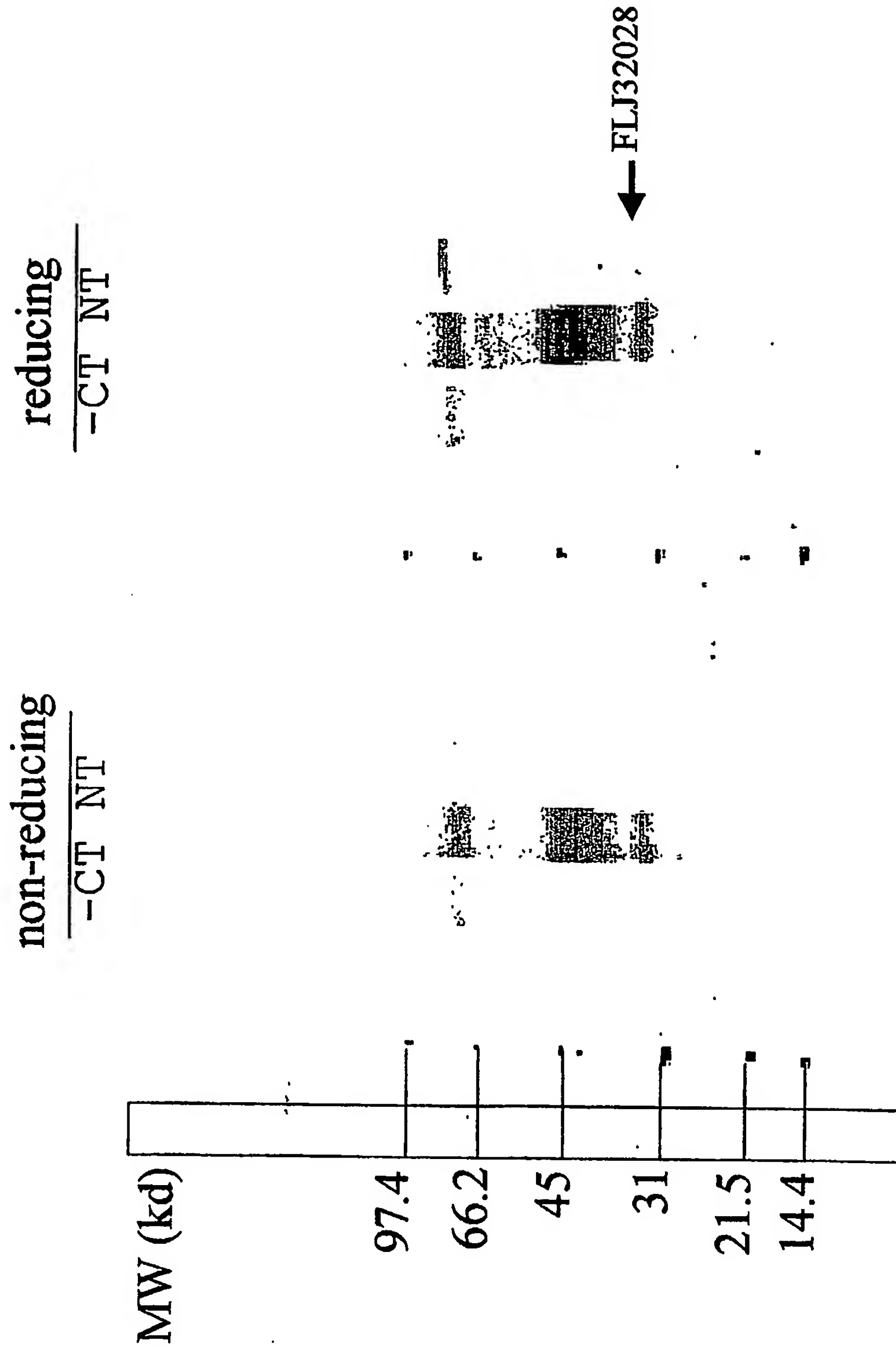


FIG. 6

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FLJ32028 polynucleotide sequence (SEQ. ID No. 2):

AGCCCGGCGCAGCATCCTGAGCGCGCCTCTGCCGAGGCGAGCGGACATG  
CAGGCTCCCCGCGCAGCCCTAGTCTTCGCCCTGGTGATCGCGCTCGTTCC  
CGTCGGCCGGGGTAATTATGAGGAATTAGAAAACCTCAGGAGATACAACTGT  
GGAATCTGAAAGACCAAATAAAGTGACTATTCCAAGCACATTTGCTGCAGTG  
ACCATCAAAGAAACATTAAATGCAAATATAAATTCTACCAACTTTGCTCCGGA  
TGAAAATCAGTTAGAGTTTATACTGATGGTGTTAATCCCATTTGATTTTATTGG  
TCCTCTTACTTTTATCCGTGGTATTCTTGCAACATACTATAAAAGAAAAAGA  
ACTAACAAGAACCTTCTAGCCAAGGATCTCAGAGTGCTTTACAGACATATGA  
ACTGGGAAGTGAAAACGTGAAAGTCCCTATTTTTGAGGAAGATACACCCTCT  
GTTATGGAAATTGAAATGGAAGAGCTTGATAAATGGATGAACAGCATGAATA  
GAAATGCCGACTTTGAATGTTTACCTACCTTGAAGGAAGAGAAGGAATCAAA  
TCACAACCCAAGTGACAGTGAATCCTAAACCTGAATGGCGCTCATGTTTTCC  
AAGAGAAGCAGCCCCTGAGGGAGTCTGCTGAGGCTGCCAACA

*FIG. 7*

FLJ32028 polypeptide sequence (SEQ. ID No. 1):

MQAPRAALVFALVIALVPVGRGNYEELNSGDTTVESERPKNKVTIPSTFAAVTIK  
TLNANINSTNFAPDENQLEFILMVLIPLILLVLLLLSVFLATYYKRKRTKQEPSSQ  
GSQSALQTYELGSENVKVPIFEEDTPSVMEIEMEELDKWMNSMNRNADFECLP  
TLKEEKESNHNPSDSES

*FIG. 8*

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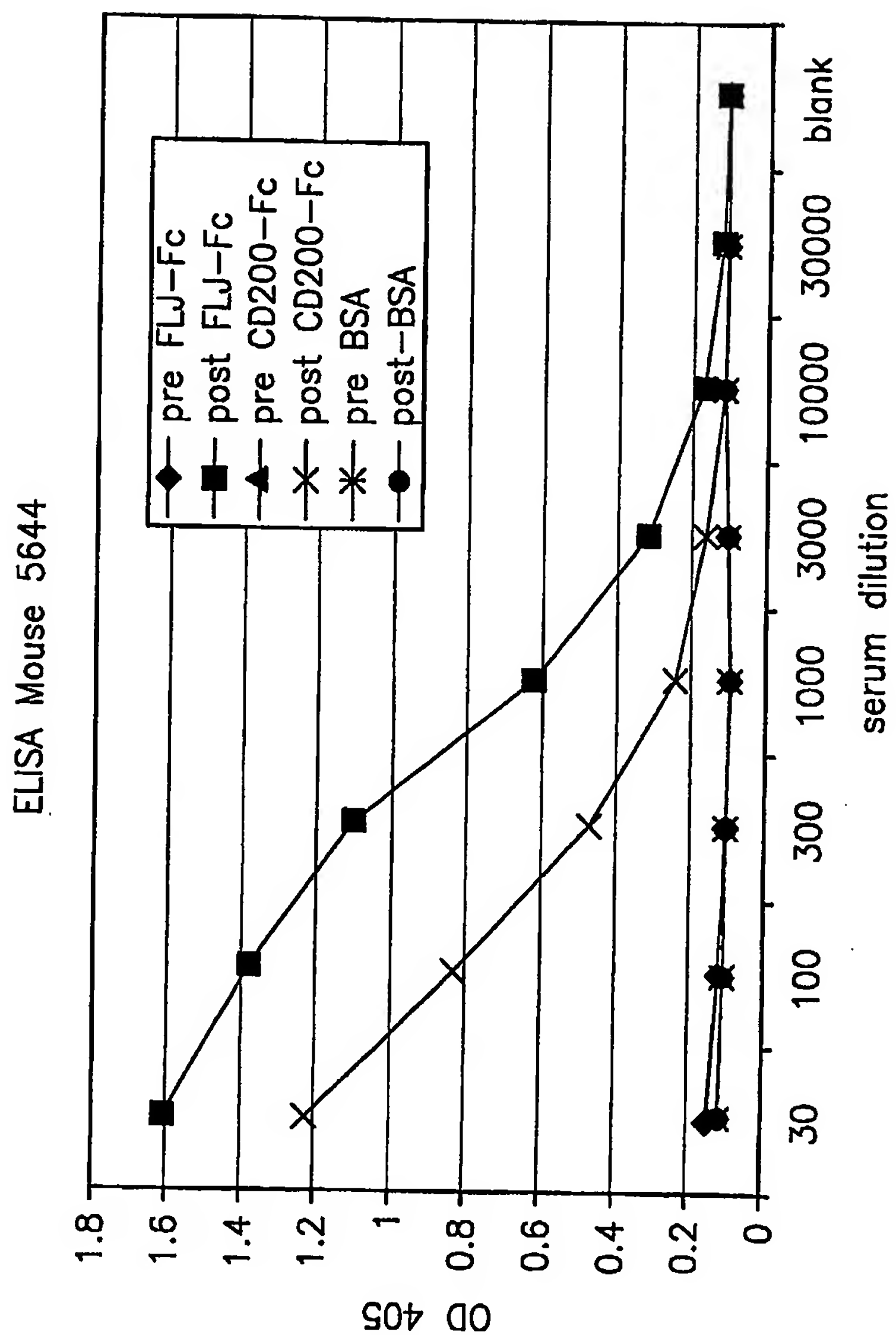
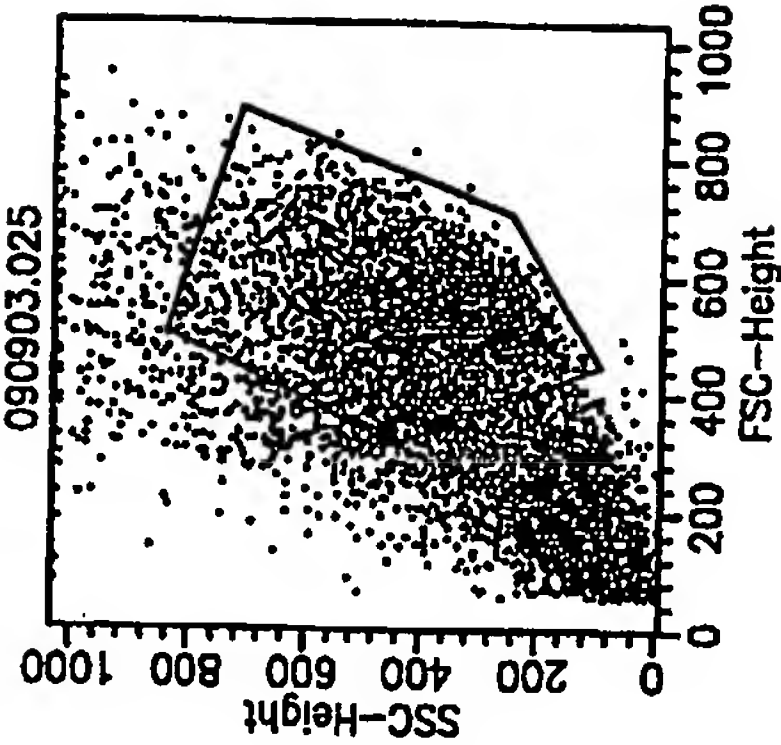


FIG. 9A

Mouse 5644



Key	Name	Parameter	Gate
▨	090903.025	FL2-H	G1
—	090903.031	FL2-H	G1
—	090903.037	FL2-H	G1
—	090903.043	FL2-H	G1
—	090903.007	FL2-H	G1
—	090903.013	FL2-H	G1
—	090903.019	FL2-H	G1
		pre	1:30/FLJ
		post	1:30/FLJ
		post	1:100/FLJ
		post	1:300/FLJ
		post	1:30/mock
		post	1:100/mock
		post	1:300/mock

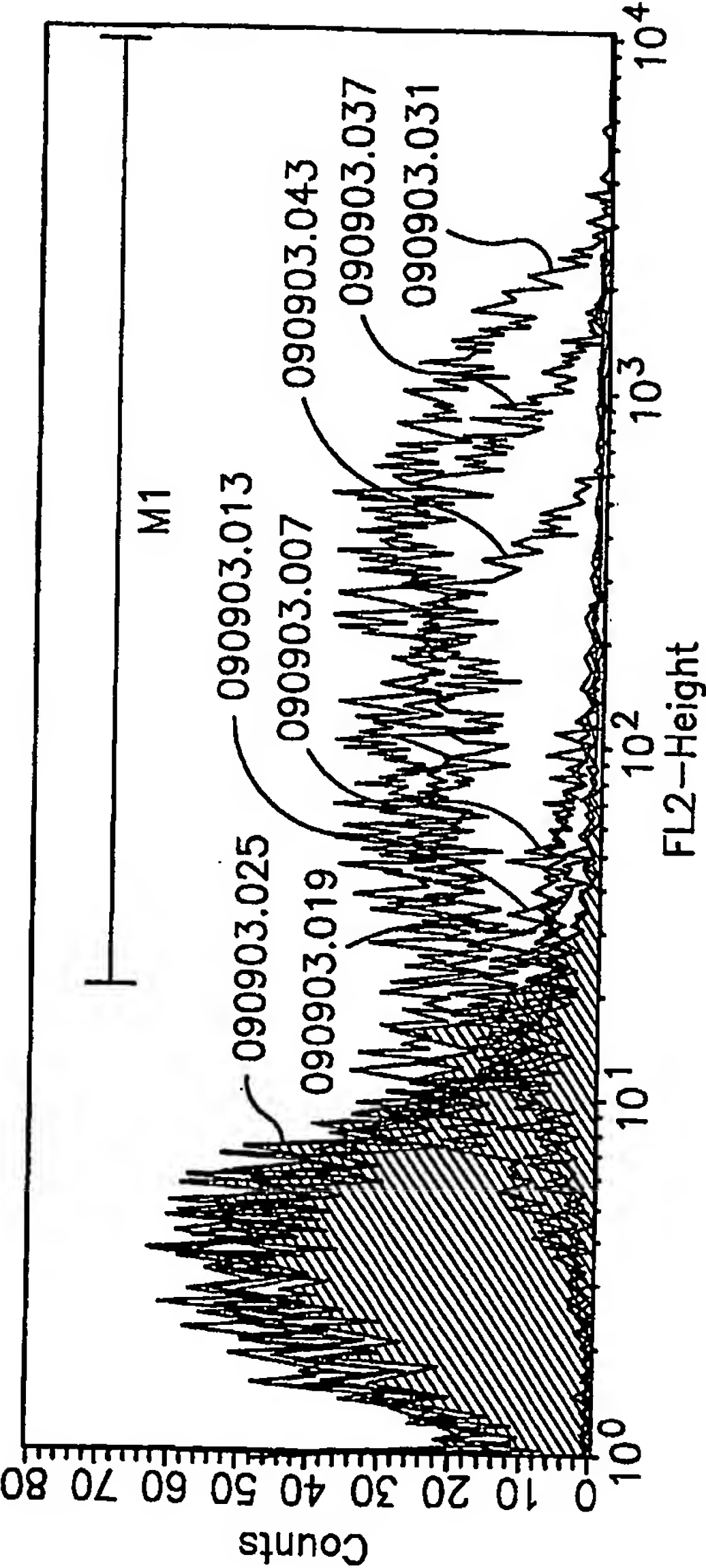


FIG. 9B

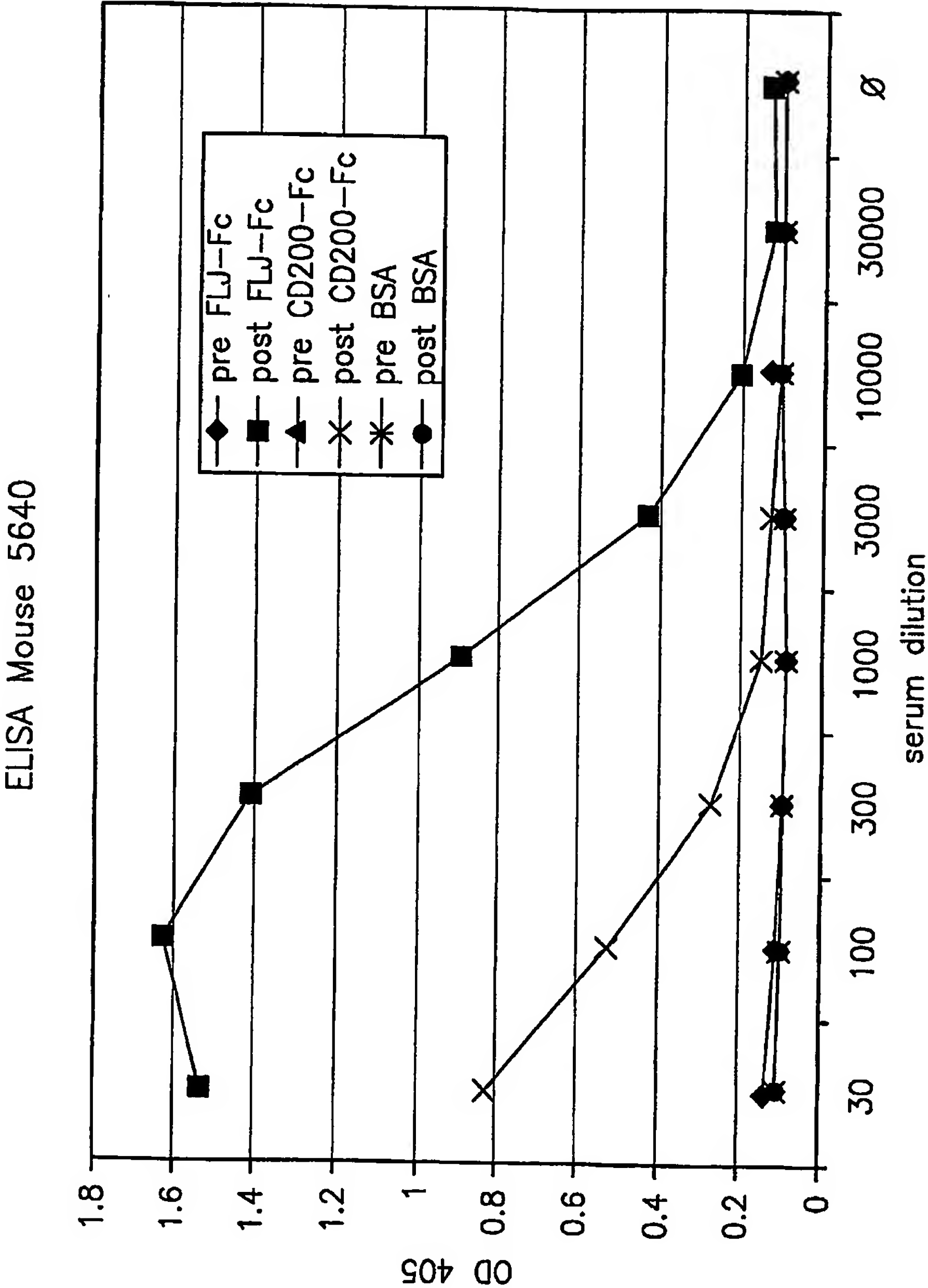
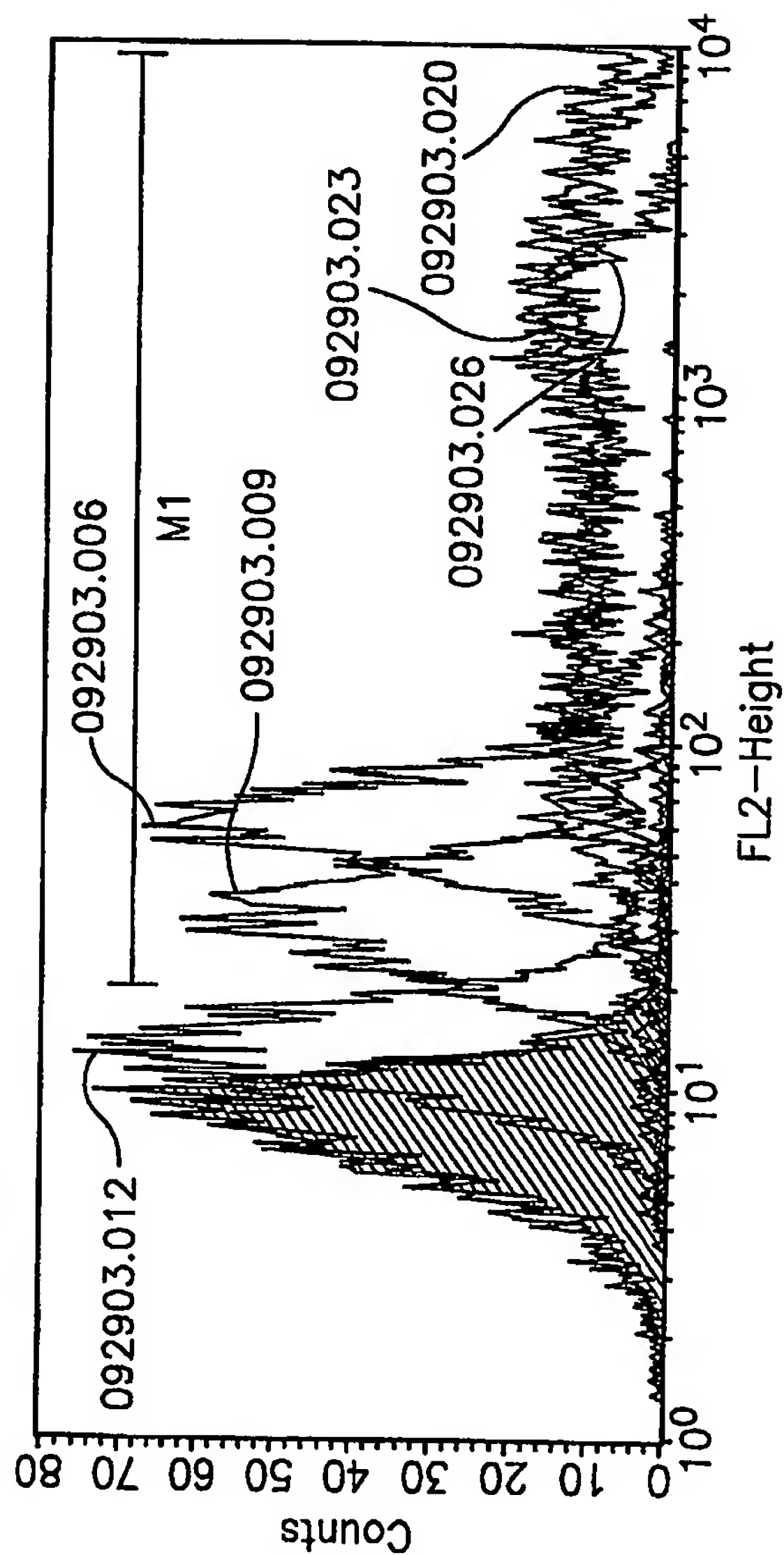
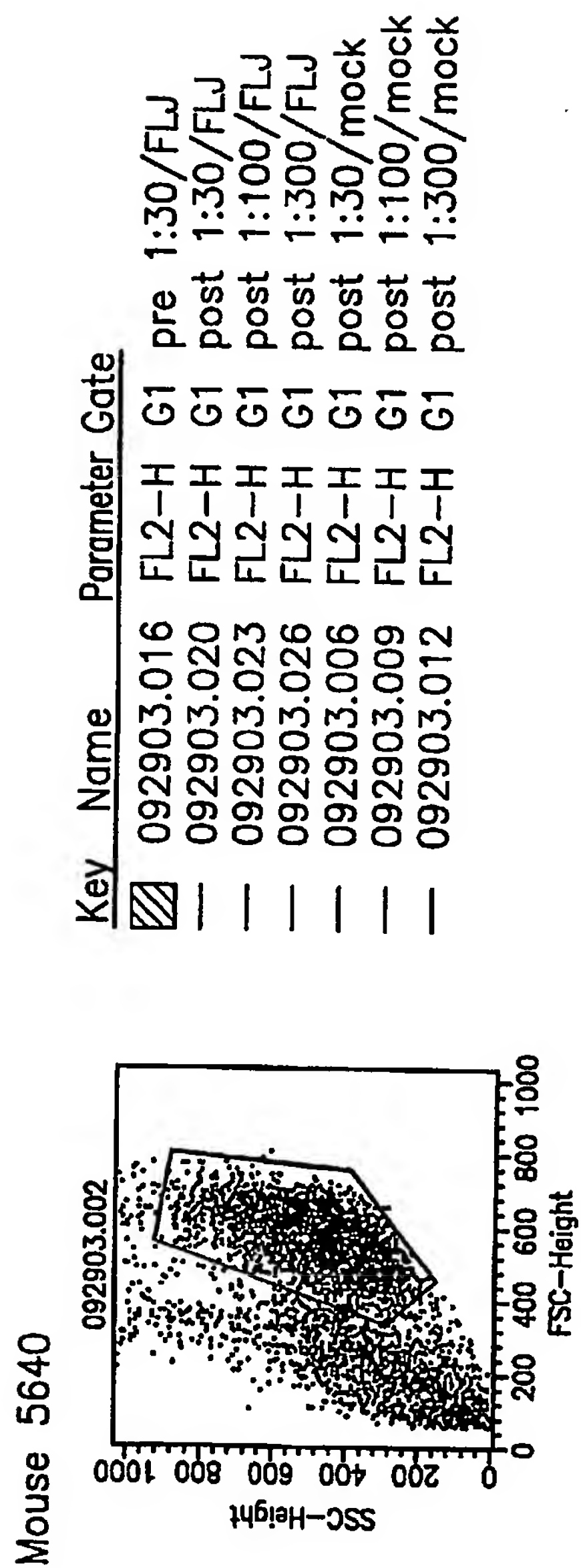


FIG. 10A



**FIG. 10B**



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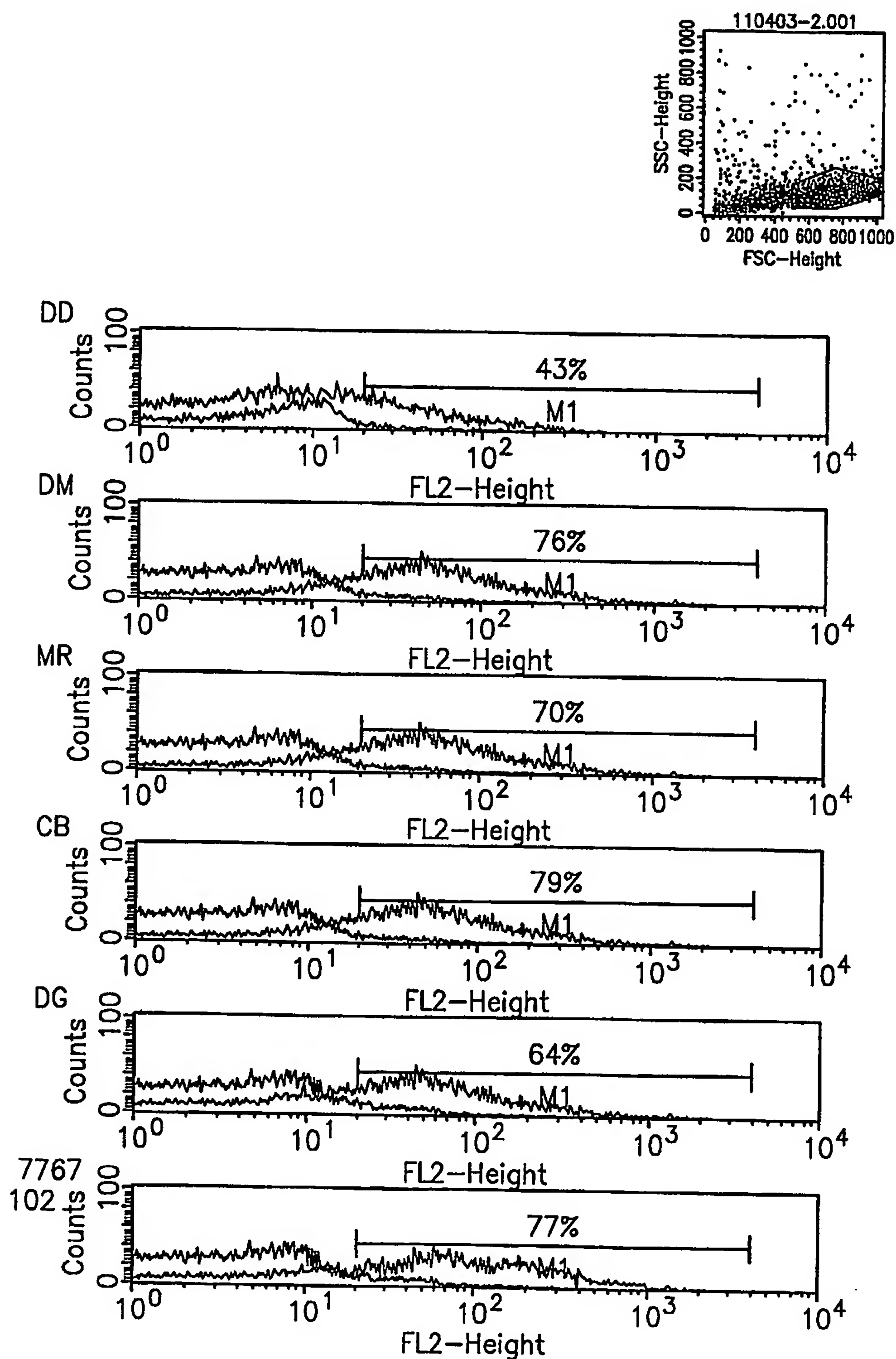


FIG. 11

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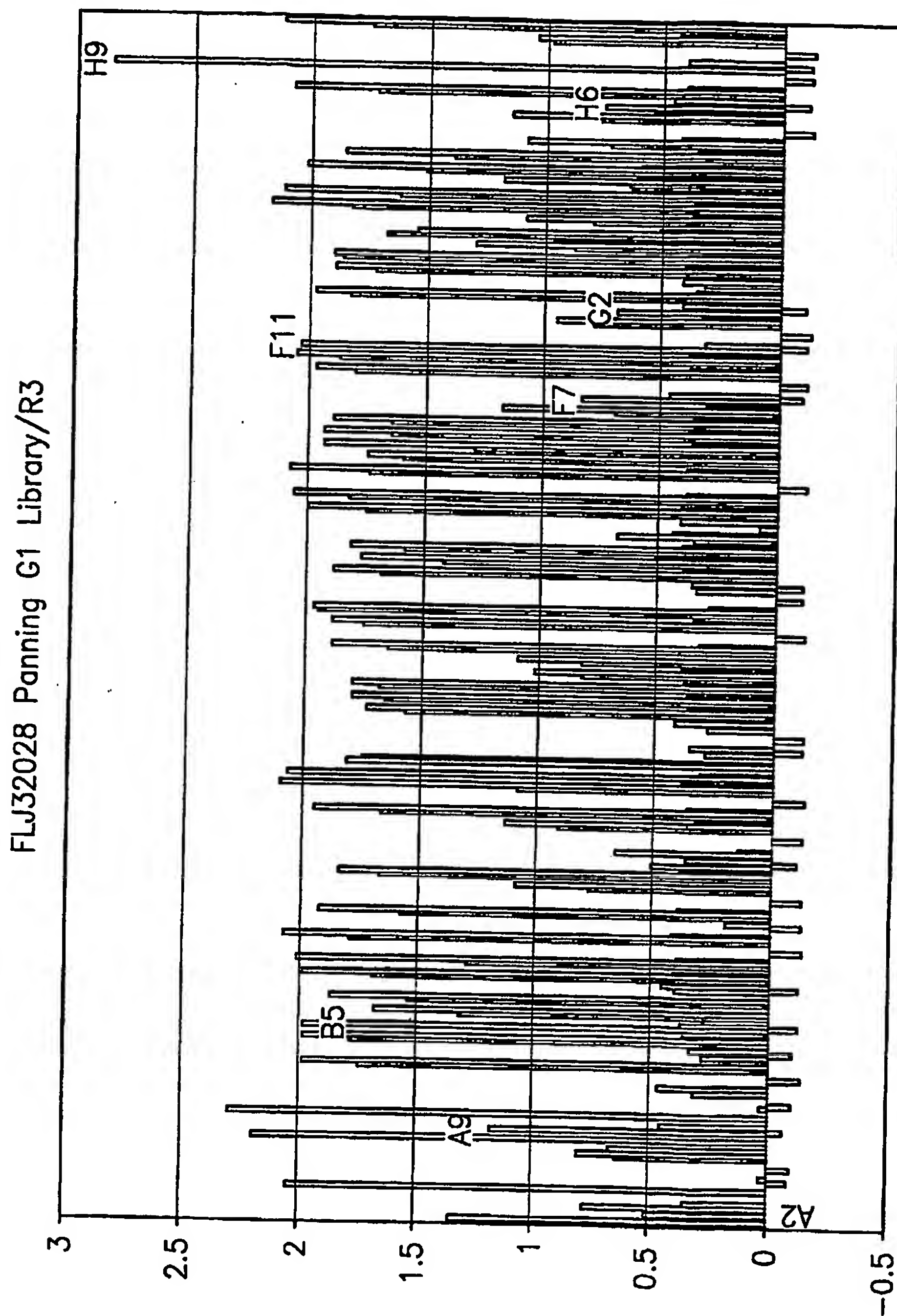
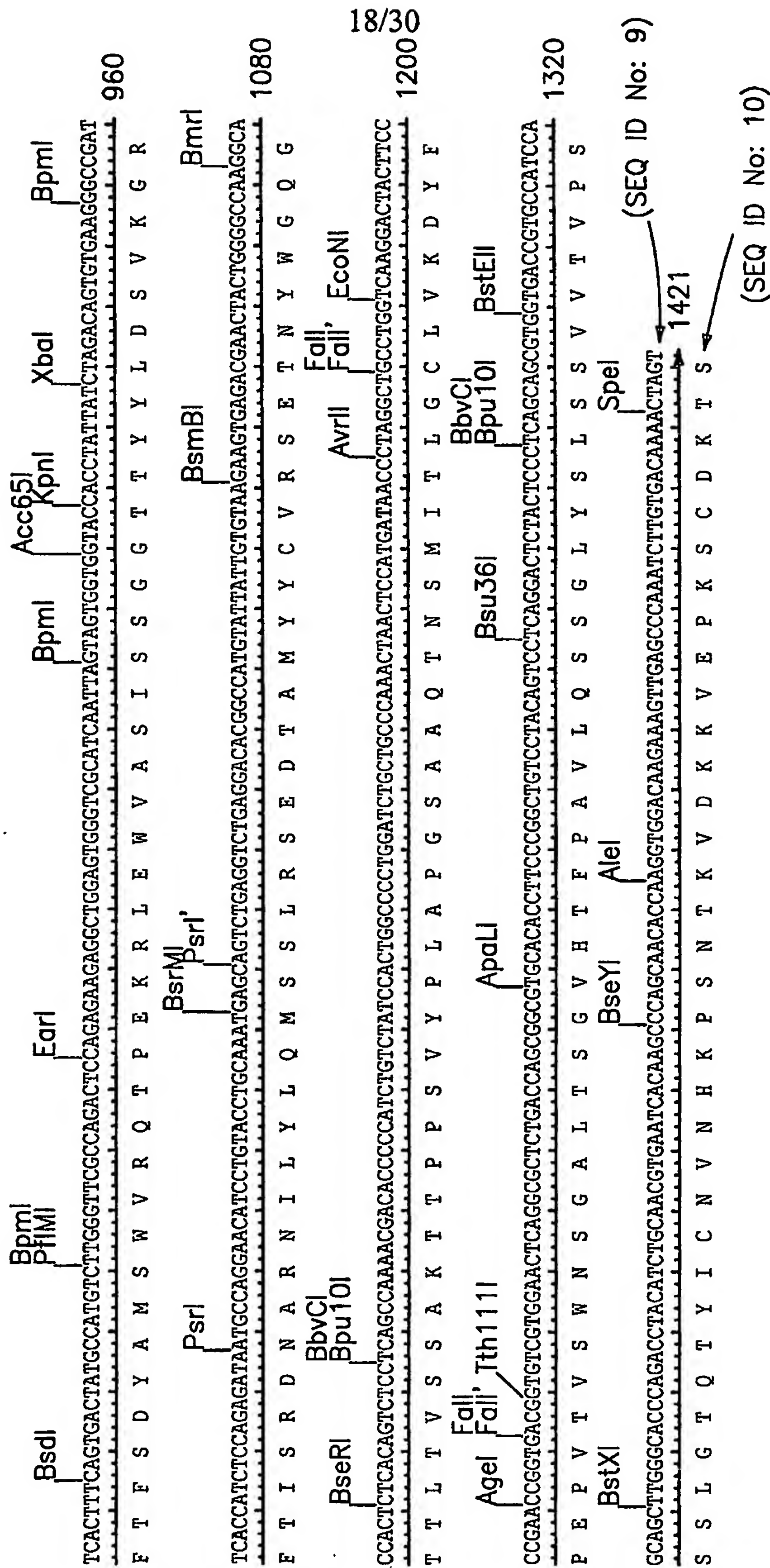


FIG. 12

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**FIG. 13**





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**FIG. 14**

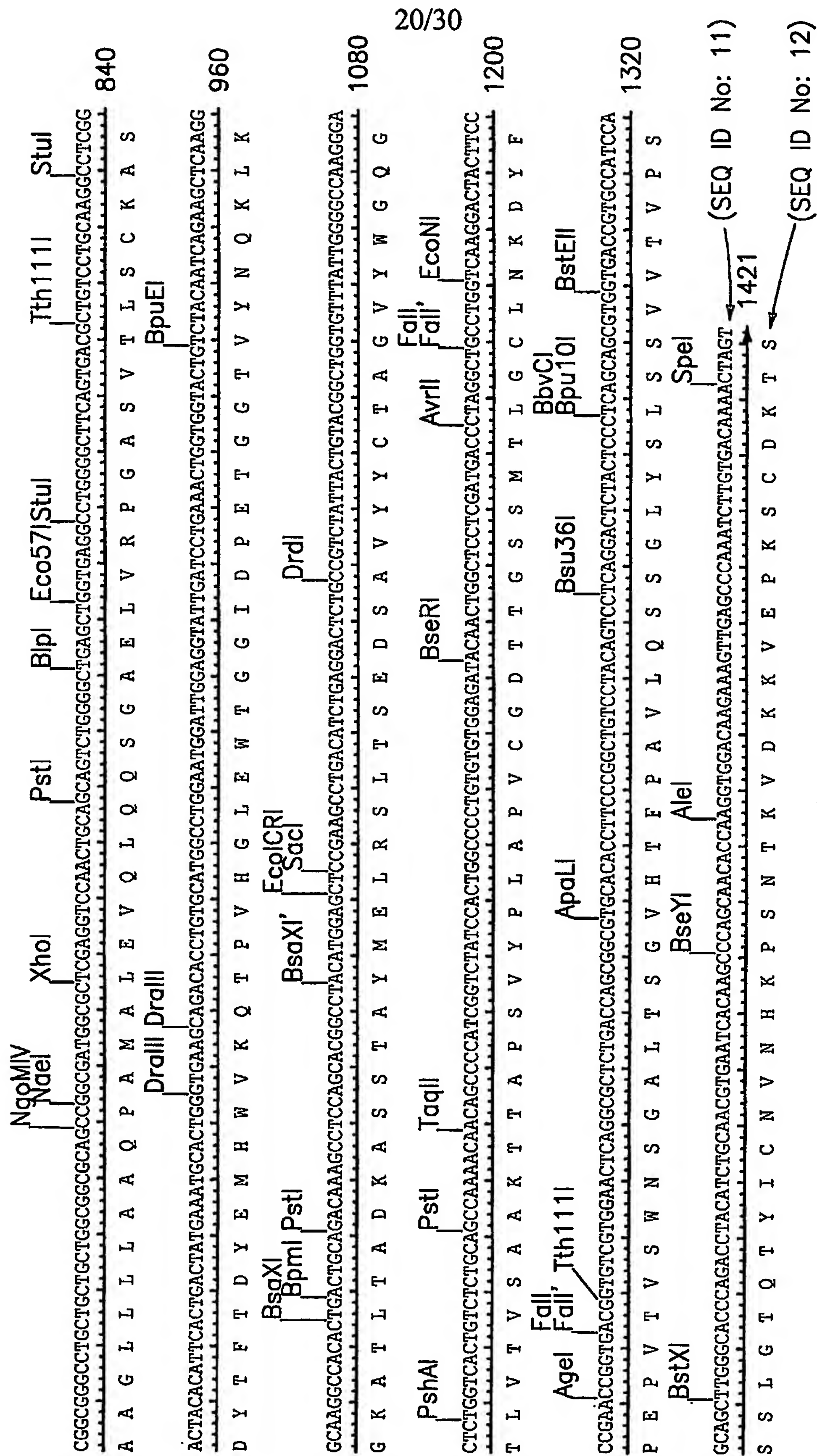


FIG. 14 (Cont.)



VL amino acid sequences of FLJ32028-specific IgG1 kappa clones from 5644 library

Clone	FR1	CDR1	FR2	CDR2
11F	DIQMTQTSSLSASLGDRVTISCRTS	QDISN-----Y LNWYQQKPDGTVKVLII	YTS	
11G	..V..AEL·SPVTS·ES·S...S·	KSLLYK-DGKT·	...L·R·GQSPQL...	FM·
6H	..V...SP...AV·V·EK·M·KS·	·SLLYSSNQKN·	·A.....GQSP·L...	WA·
9H	..V·S·SP...AV·V·EK·M·KS·	·SLLYSSNQKN·	·A.....GQSP·L...	WA·
9A	·VV...PL·PV...QAS...S·	·S·VHS-NGNT·	·E·L...GQSP·L...	KV·
2G	·VV...PL·PV...QAS...S·	·S·VHS-NGNT·	·E·L...GQSP·L...	KV·
7F	·VL...PL·PV...QAS...S·	·S·VHS-NGNT·	·E·L...GQSP·L...	KV·

ELISA ODs:				
FR3		CDR3	FR4	ELISA ODs: FLJ/ Fc/ Fab
RLHSGVPSRFSGSGTDYSLTINNLEQED	DIATYFC	QQGNTLPFTFGSG	TKLEIKR	2.14/0.12/0.46 (SEQ ID NO: 13)
TRAP...SD...I...FT·E·SRVKA·	·VGV·Y·	·LVEY·L...A·	...L...	1.98/0.14/0.41 (SEQ ID NO: 14)
TRE...D·T...FT...SSVKA·	L·V·Y·	·YYSY·L...A·	...L...	0.86/0.12/0.61 (SEQ ID NO: 15)
ARG...D·T...FT...SSVKA·	L·V·Y·	·YYSY·L·I·A·	...L...	2.95/0.11/0.56 (SEQ ID NO: 16)
NRF...D...FT·K·SRV·A·	·LGV·Y·	F·SHV·L...A·	...L...	1.30/0.17/0.61 (SEQ ID NO: 17)
NRF...D...FT·K·SRV·A·	·LGV·Y·	F·SHV·L...A·	...L...	0.80/0.12/0.57 (SEQ ID NO: 17)
NRF...D...FT·K·SRV·A·	·LGV·Y·	F·SHV·L...A·	...L...	0.95/0.13/0.62 (SEQ ID NO: 17)

FR: framework region; CDR: complementarity determining region. Dots indicate identities with the clone 11F sequence. Dashes indicate gaps in the alignment. ELISA ODs are given for binding of the phage antibody clones to FLJ32028-Fc fusion protein(FLJ), to negative control Fc fusion protein(Fc), and to Anti-F(ab')<sub>2</sub> (Fab).

FIG. 15

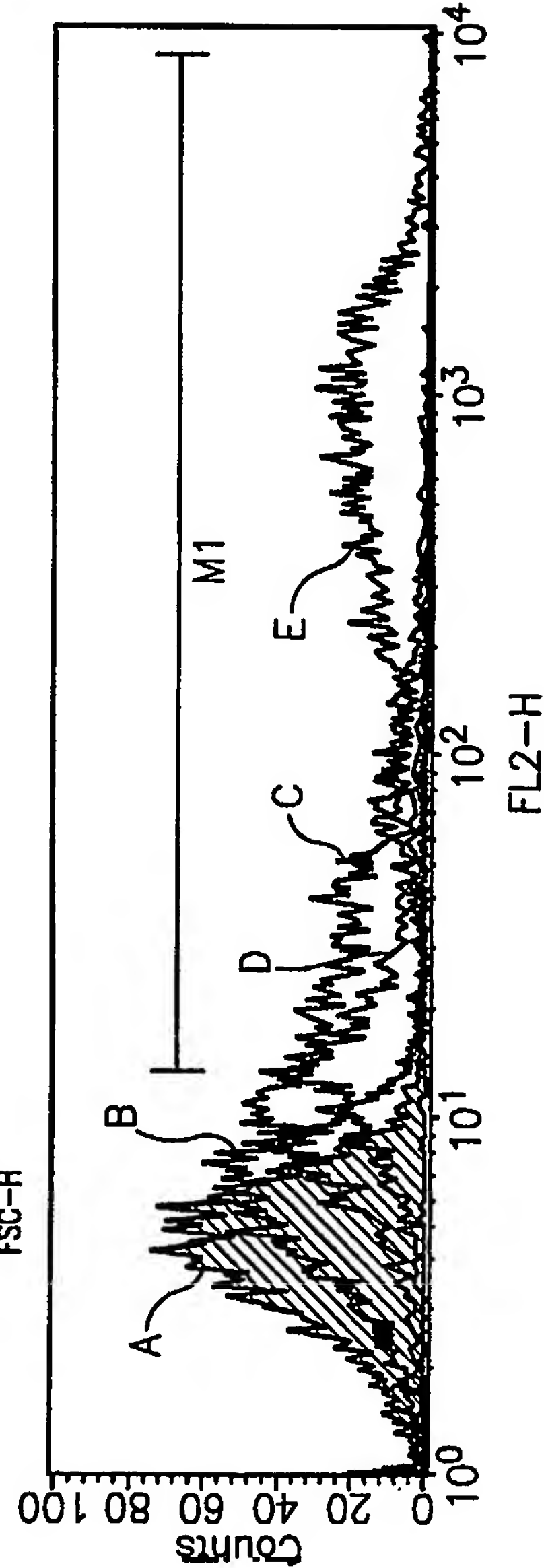
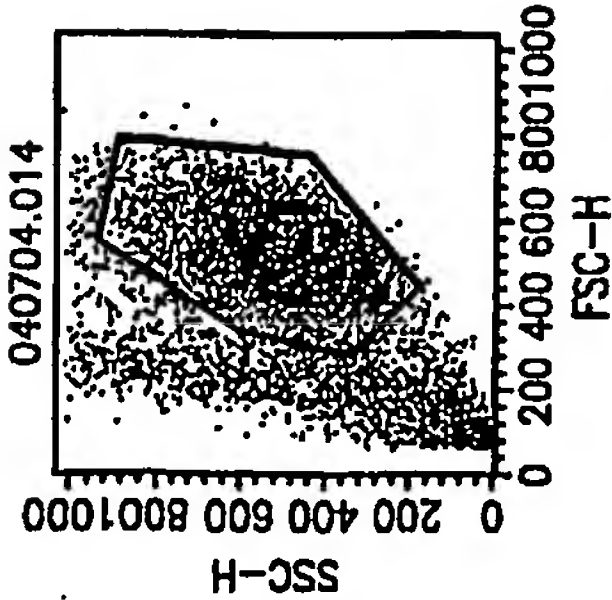
VH amino acid sequences of FLJ32028-specific IgG1 kappa clones from 5644 library

Clone	FR1	CDR1	FR2	CDR2
11F	LEVQLQQSGAELVRPGASVTLCKAS	GYTFDYEMH	WVKQTPVHGLEWIG	GIDPEIGGTVYNQKFKG
11G	.....	D.....	.....	.....T.....L.....
5B	.....	.....V.....	.....Q.....D.....	.....S.....A.....
6H	.....K.....	.....FNIK.....TYIN.....	.....R.....EQ.....	.....R.....ANN.....N.....DP.....Q.....
9H	.....F.....	.....FNIK.....TY.....N.....	.....I.....R.....EQ.....	.....M.....AN.....N.....Q.....DP.....Q.....
9A	.....K.....VE.....GG.....	.....K.....G.....LK.....A.....	.....F.....S.....A.....S.....	.....VA.....S.....S.....SG.....T.....Y.....LDSV.....
2G	.....AK.....VE.....GG.....	.....K.....G.....LK.....A.....	.....F.....S.....A.....S.....	.....VA.....S.....S.....SG.....T.....Y.....LDSV.....
7F	.....K.....VE.....GG.....	.....K.....G.....LK.....A.....	.....F.....S.....A.....S.....	.....VA.....S.....S.....SG.....T.....Y.....LDSV.....

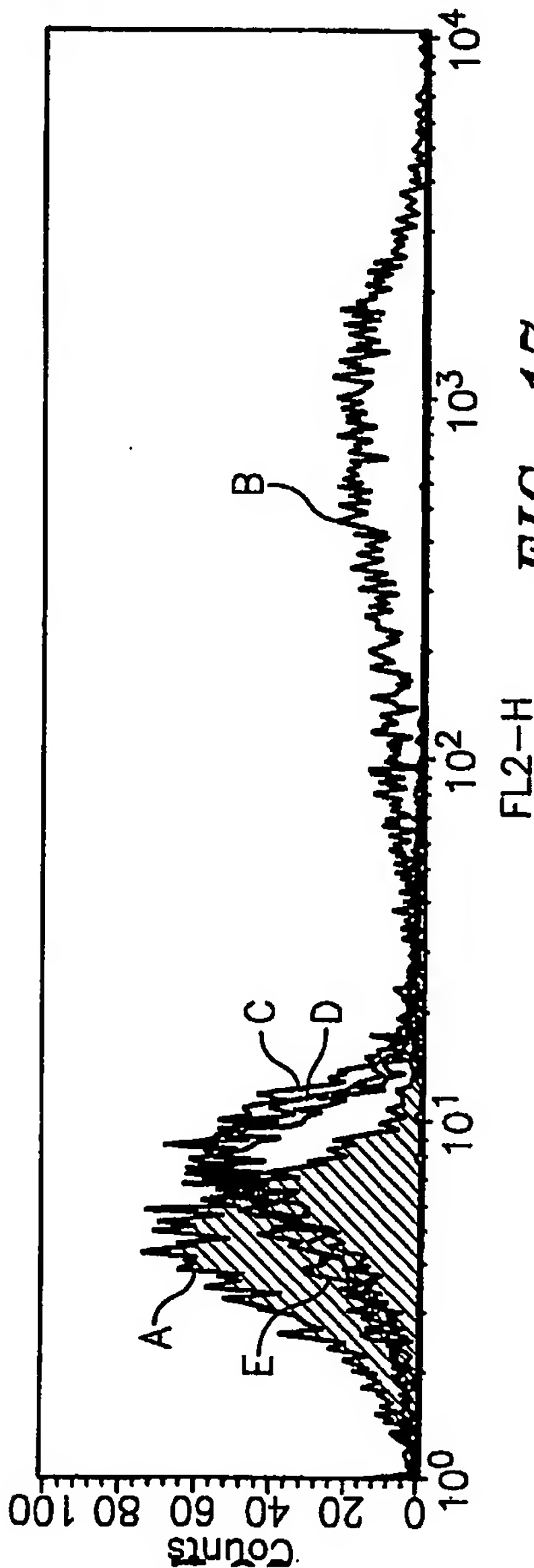
ELISA ODs:				
FR3	CDR3	FR4	FLJ/ Fc/ Fab	
KATLTADKSSGTAYMELRSLTSEDSAVYICTS	F---AY	WGQGLTVTSA	2.14/0.12/0.46	(SEQ ID NO: 18)
.....A.S.....	G---V.	.....	1.98/0.14/0.41	(SEQ ID NO: 19)
.....R.....	G---AD	.....F.	1.84/0.11/0.53	(SEQ ID NO: 20)
...I...TP.N...LQ.S.....	TD.....V.	GGYFD.	0.86/0.12/0.61	(SEQ ID NO: 21)
...I...T.N...LQ.S.....	T.....	GGYFD.	2.95/0.11/0.56	(SEQ ID NO: 22)
RF.ISR.NARNIL.LQMS..R...T.M...VR	S-ETN.	.....TL.....	1.30/0.17/0.61	(SEQ ID NO: 23)
RF.ISR.NARNIL.LQMS..R...T.M...VR	S-ETN.	.....TL.....	0.80/0.12/0.57	(SEQ ID NO: 24)
RF.ISR.NARNIL.LQMS..R...T.M...VR	S-ETN.	.....TL.....	0.95/0.13/0.62	(SEQ ID NO: 23)

FR: framework region; CDR: complementarity determining region. Dots indicate identities with the clone 11F sequence. Dashes indicate gaps in the alignment. ELISA ODs are given for binding of the phage antibody clones to FLJ32028-Fc fusion protein(FLJ), to negative control Fc fusion protein(Fc), and to Anti-F(ab')<sub>2</sub> (Fab).

FIG. 16



Key	Name	Parameter	Gat
▨	040704.014	FL2-H	G1 A
—	040704.022	FL2-H	G1 B
—	040704.020	FL2-H	G1 C
—	040704.024	FL2-H	G1 D
—	040704.019	FL2-H	G1 E



Key	Name	Parameter	Gat
▨	040704.014	FL2-H	G1 A
—	040704.018	FL2-H	G1 B
—	040704.021	FL2-H	G1 C
—	040704.017	FL2-H	G1 D
—	040704.023	FL2-H	G1 E

FIG. 17

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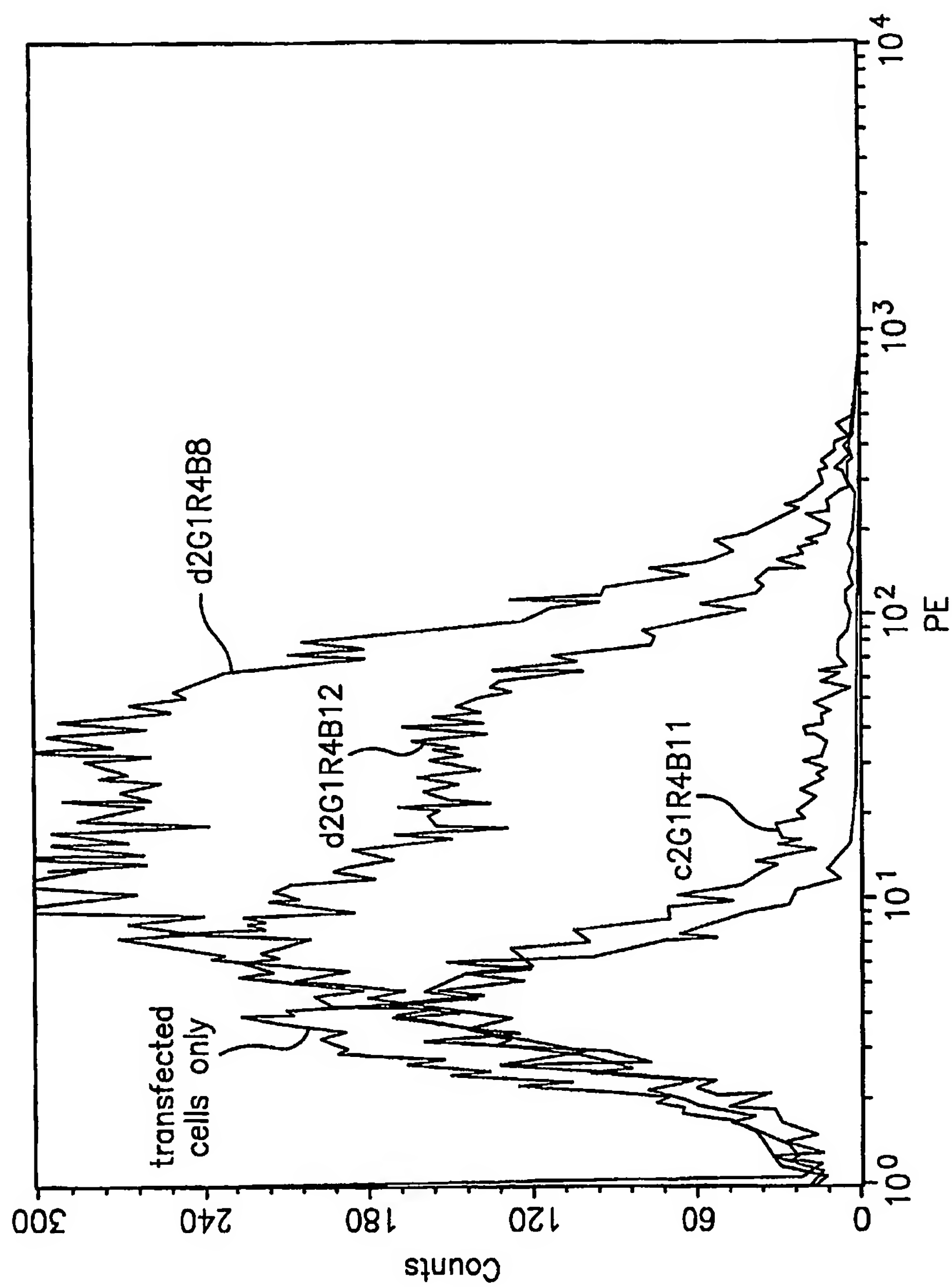


FIG. 18A

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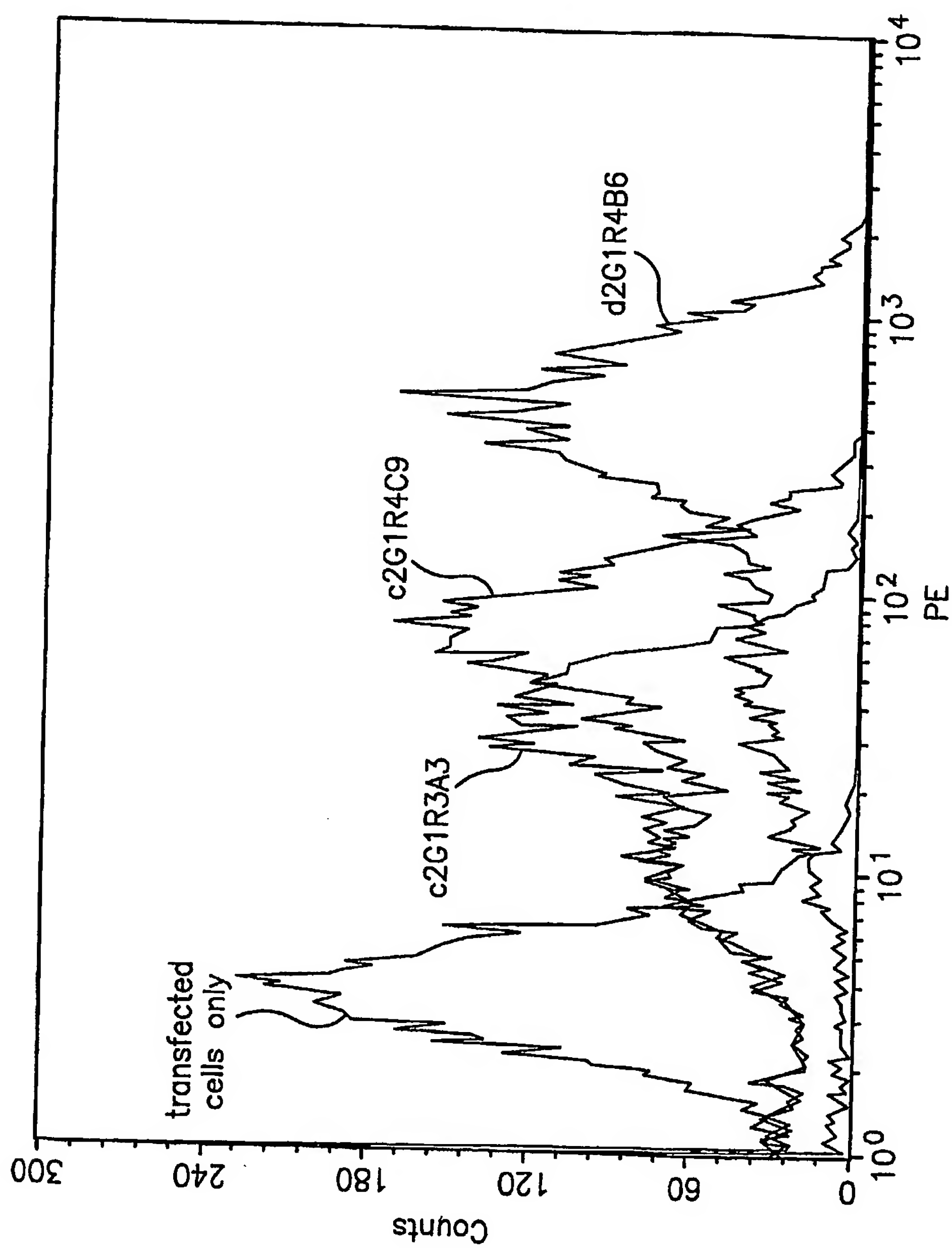


FIG. 18B

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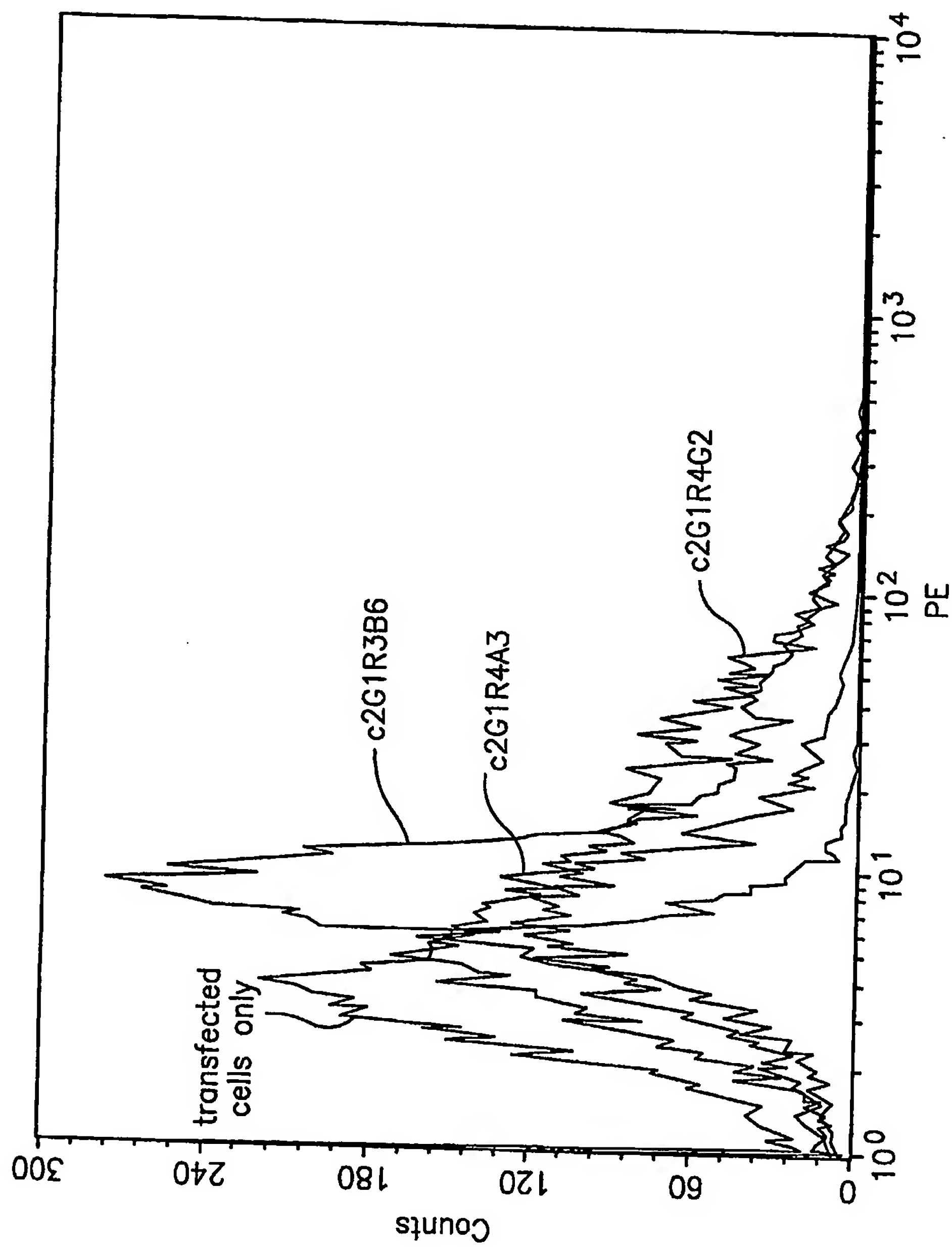


FIG. 18C



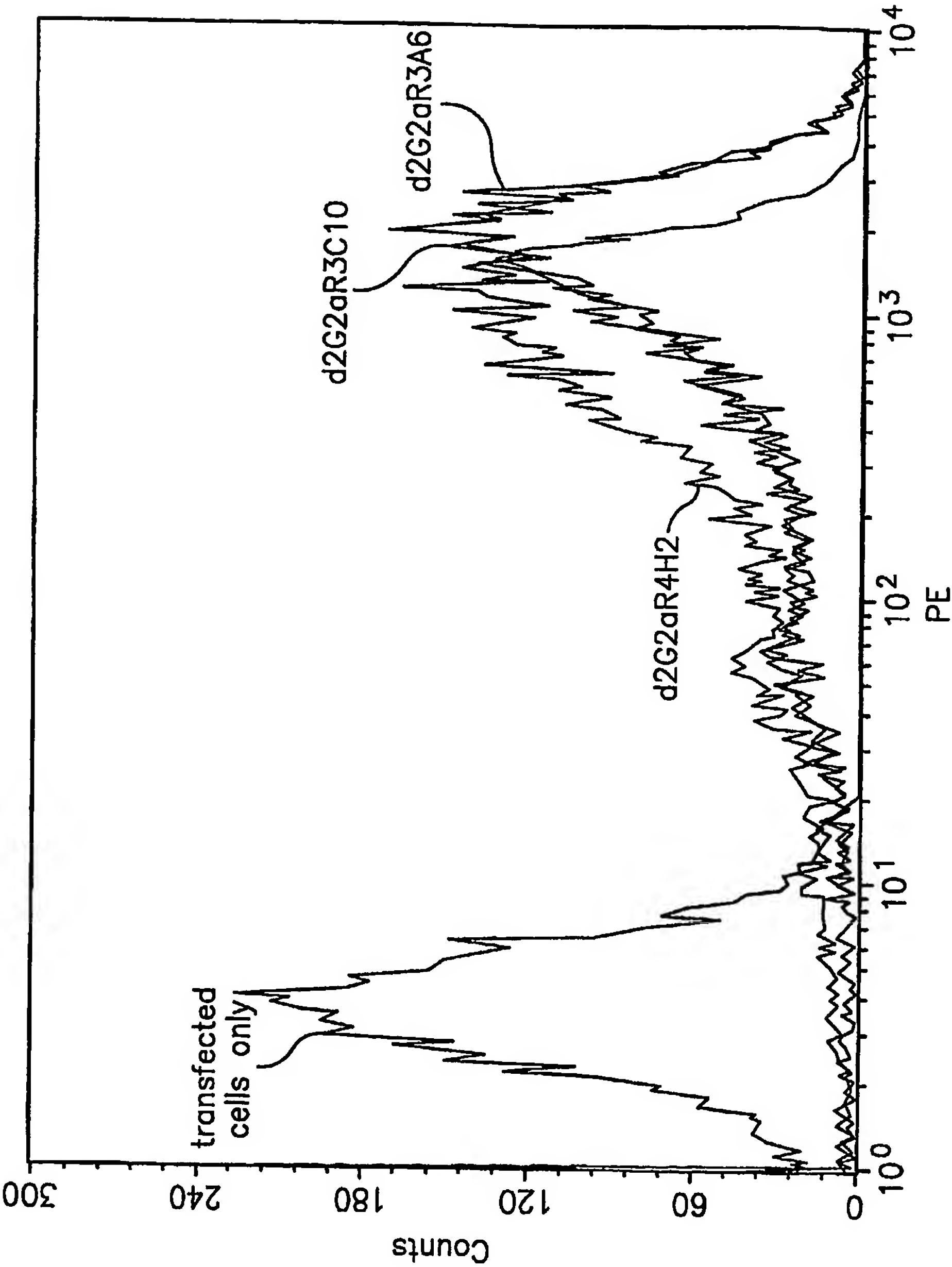


FIG. 18D

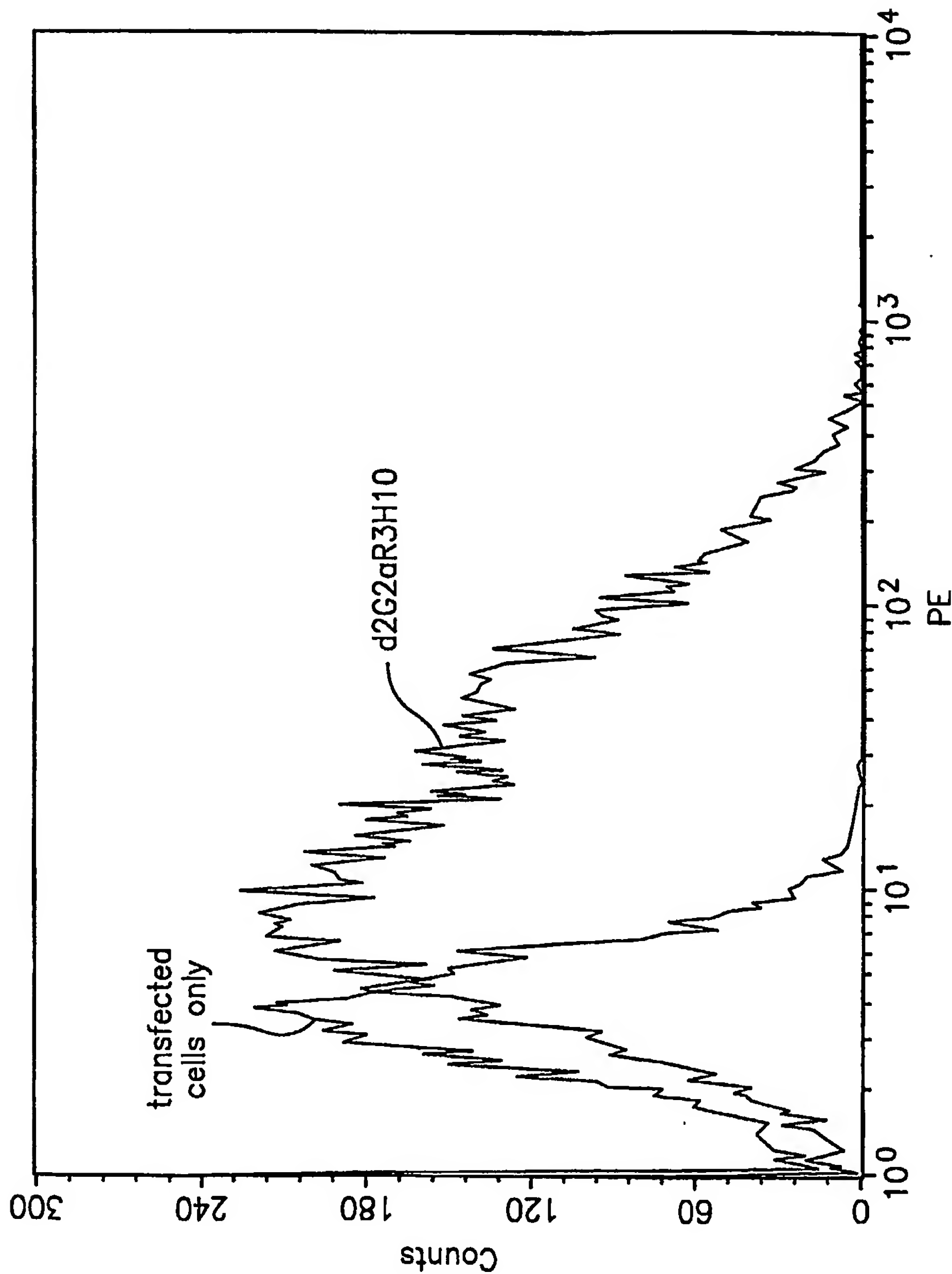


FIG. 18E

FLJ32028 binding clones

Fab	FR1	CDR1	FR2	CDR2
c2G1R3A3	LEVQLVESGGGLVQPKGSLKLSCAAS	GFNTFTYAMN	WVRQSPGKGLEWVA	RIRTKSNNYATYYADSVKD
c2G1R3A12	.....	.....	...A.....	...S.....
c2G1R3C2	.....	.....	...A.....	...S.....
c2G1R3E3	.....	.....	...A.....	...S.....
c2G1R3F5	...K.....	.....	...A.....	...S.....
c2G1R3F6	...K.....	.....	...A.....	...S.....
d2G1R4B6	.....	.....	...A.....	...S.....
c2G1R4C9	.....	.....	...A.....	...S.....
c2G1R3B6	LEVQLQSQSGAELAKPGASVKMSCKAS	GYTFTNSWIH	WVKQRPQGQGLEWIG	YIHPGPGYTEYNQNFKD
c2G1R4G2	LEVQLKQSGAELVKPGASVKLSCTAS	GFNIKDTYMN	WVKQRPEQGQGLEWIG	GIDPANDNTEYVPKFQG
C2G1R4A3	...Q.....	.....	.....	.....
d2G1R4B12	LEVQLQSQSGAELVRPGASVTLCKAS	GYTFTDYEMH	WVKQTPVHGQGLEWIG	GIDPETGGTVYNQKFKG
d2G1R4B8	.....	.....	.....	.....
d2G2aR3A6	LEVQLVESGGGLVQPKGSLKLSCAAS	GFNTFTYAMN	WVRQAPGKGLEWVA	RIRTKSNNYATYYADSVKD
d2G2aR3C10	.....	.....	.....	.....
d2G2aR4A12	.....	.....	.....	.....
d2G2aR4G6	.....	.....	.....	.....
d2G2aR4H2	.....	.....	.....	.....
d2G2aR3H10	LEVQLQSQSGAELVRPGASVTLCKAS	GYTFTDYEMH	WVKQTHVHGQGLEWIG	GIDPETGGTVYNQKFKG

FIG. 19

Fab	ELISA/FACS				SEQ ID NO:
	FR3	CDR3	FR4	(geo mean)	
c2G1R3A3	RFSVSRDDSQSMLYLQMNLLKTEDTAMYYCVR	HEGDWFAY	WGQGTLLTVSE	0.582/20.46	24
c2G1R3A12	..TI.....	.....	.....A	0.492/16.02	25
c2G1R3C2	..TI.....	.....	.....A	0.481/9.68	25
c2G1R3E3	..TI.....	.....	.....A	0.507/12.67	25
c2G1R3F5	..TI.....	.....	.....A	0.356/12.61	26
c2G1R3F6	..TI.....	.....	.....A	0.446/14.7	26
d2G1R4B6	..TI.....	.....	.....A	0.980/156	25
c2G1R4C9	..TI.....	..N....	.....A	0.360/24.62	27
c2G1R3B6	KATLTADKSSSTAYIQLSSLTSEDSAVYYCIR	GGDWGY	WGQGTSLTVSS	1.184/10.6	28
c2G1R4G2	RATITADTSSNTAYLQLRSLTSDDTAVYYCVT	GGYFDY	WGQGTLLTVSS	2.412/11.08	29
c2G1R4A3	.....	.....	.....	0.743/5.81	30
d2G1R4B12	KATLTADKSSSTAYMELRSLTSEDSAVYYCTR	WDY	WGQGTLLTVSS	1.426/13.8	31
d2G1R4B8	.....	.....	.....	1.415/17.84	31
d2G2aR3A6	RFTISRDDSQSMLYLQMNLLKTEDTATYYCVR	QGENRFAY	WGQGTLLTVSA	0.622/552.3	32
d2G2aR3C10	.....	.....	.....	0.574/535	32
d2G2aR4A12	.....	.....	.....	0.592/366	32
d2G2aR4G6	.....	.....	.....	0.184/164	32
d2G2aR4H2	.....	.....	.....	0.551/301.8	32
d2G2aR3H10	KATLTADKSSSTAYMELRSLTSEDSAVYYCTS	SLP	WGQGTLLTVSA	0.740/16.41	33
negative control					

Top sequence in each group is used as a reference for others in the same group. Only the amino acids different from the reference sequence are shown in each sequence and the same amino acids are indicated by dots. ELISA is OD405 reading at 60 min to the FLJ32028 coated wells (4 µg/ml) and FACS (geo mean ) is showing geometric mean.

FIG. 19 (Cont.)